Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED   CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>**
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of "Artificial" (NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

OIPE

```
          RAW SEQUENCE LISTING              DATE: 04/05/2001
          PATENT APPLICATION:  US/09/805,694   TIME: 08:05:50

          Input Set : A:\BB1432 US NA Seq Listing.txt
          Output Set: N:\CRF3\04052001\I805694.raw
```

Does Not Comply
Corrected Diskette Needed

```
     3 <110> APPLICANT: Kinney, Anthony
     5 <120> TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans
     7 <130> FILE REFERENCE: BB1432 US NA
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/805,694
C--> 10 <141> CURRENT FILING DATE: 2001-03-14
    12 <150> PRIOR APPLICATION NUMBER: 60/189,823
W--> 13 <151> PRIOR FILING DATE: (16 MARCH 2000)  2000-03-16
    15 <160> NUMBER OF SEQ ID NOS: 16
    17 <170> SOFTWARE: Microsoft Office 97
```

ERRORED SEQUENCES

```
    230 <210> SEQ ID NO: 5
    231 <211> LENGTH: 494
    232 <212> TYPE: DNA
    233 <213> ORGANISM: Glycine max
    235 <400> SEQUENCE: 5
E--> 236 acacagctng cacatattac atacacgtga atcactaatt aagccatgga gaagaaatca  60
    237 atagctgggt tgtgcttcct cttccttgtt ctctttgttg ctcaagaagt tgtggtgcaa 120
    238 actgaggcaa agacttgcga gaacctggct gatacataca ggggtccatg cttcaccact 180
    239 ggcagctgcg atgatcactg caagaacaaa gagcacttgc tcagaggcag atgcagggac 240
    240 gattttcgct gttggtgcac caaaaactgt taaatggatc cattcactcc aacgtgaaga 300
    241 agatgcatgc agcgctattt tataaaagat acaactacta tatactatat ataataagac 360
E--> 242 tgggcgctgc atcaatgacc ctatgtanta tnntatatat tattaccgat gtcaagaact 420
E--> 243 atagatgcat gtactgtgca taacggctga gttatgtcon tangttanga ataaaaataa 480
    244 agtgctgttg ttgc                                                    494
```

see item 10
on Erro
Summary Sheet

VERIFICATION SUMMARY   DATE: 04/05/2001
PATENT APPLICATION: US/09/805,694   TIME: 08:05:52

Input Set : A:\BB1432 US NA Seq Listing.txt
Output Set: N:\CRF3\04052001\I805694.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:236 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
M:340 Repeated in SeqNo=5